

## SEQUENCE LISTING

<110> Merck & Co., Inc.  
Istituto di Ricerche di Biologia Molecolare P. Angeletti S.p.A.

<120> HCV REPLICONS CONTAINING NS5B FROM  
GENOTYPE 2B

<130> 21564Y PCT

<150> 60/517,605  
<151> 2003-11-05

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 591  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> modified NS5B

<221> VARIANT  
<222> (5)...(5)  
<223> Xaa = threonine or serine

<221> VARIANT  
<222> (24)...(24)  
<223> Xaa = asparagine or serine

<221> VARIANT  
<222> (31)...(31)  
<223> Xaa = methionine or isoleucine

<221> VARIANT  
<222> (376)...(376)  
<223> Xaa = isoleucine or leucine

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1 5 10 15  
Glu Glu Glu Lys Leu Pro Ile Xaa Pro Leu Ser Asn Ser Leu Xaa Arg  
20 25 30  
Phe His Asn Lys Val Tyr Ser Thr Thr Ser Arg Ser Ala Ser Leu Arg  
35 40 45  
Ala Lys Lys Val Thr Phe Asp Arg Val Gln Val Leu Asp Ala His Tyr  
50 55 60  
Asp Ser Val Leu Gln Asp Val Lys Arg Ala Ala Ser Lys Val Ser Ala  
65 70 75 80  
Arg Leu Leu Thr Val Glu Glu Ala Cys Ala Leu Thr Pro Pro His Ser  
85 90 95

Ala Lys Ser Arg Tyr Gly Phe Gly Ala Lys Glu Val Arg Ser Leu Ser  
     100                       105                       110  
 Arg Arg Ala Val Asn His Ile Arg Ser Val Trp Glu Asp Leu Leu Glu  
     115                       120                       125  
 Asp Gln His Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val  
     130                       135                       140  
 Phe Cys Ile Asp Pro Thr Lys Gly Gly Lys Lys Pro Ala Arg Leu Ile  
     145                       150                       155                       160  
 Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr  
     165                       170                       175  
 Asp Ile Ala Gln Lys Leu Pro Lys Ala Ile Met Gly Pro Ser Tyr Gly  
     180                       185                       190  
 Phe Gln Tyr Ser Pro Ala Glu Arg Val Asp Phe Leu Leu Lys Ala Trp  
     195                       200                       205  
 Gly Ser Lys Lys Asp Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe  
     210                       215                       220  
 Asp Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr  
     225                       230                       235                       240  
 Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu  
     245                       250                       255  
 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Thr Asn Ser Lys Gly Gln  
     260                       265                       270  
 Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser  
     275                       280                       285  
 Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys  
     290                       295                       300  
 Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu  
     305                       310                       315                       320  
 Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu  
     325                       330                       335  
 Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp  
     340                       345                       350  
 Leu Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser  
     355                       360                       365  
 Asn Val Ser Val Ala Leu Asp Ser Arg Gly Arg Arg Arg Tyr Phe Leu  
     370                       375                       380  
 Thr Arg Asp Pro Thr Thr Pro Xaa Thr Arg Ala Ala Trp Glu Thr Val  
     385                       390                       395                       400  
 Arg His Ser Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Gln Tyr Ala  
     405                       410                       415  
 Pro Thr Ile Trp Val Arg Met Val Ile Met Thr His Phe Phe Ser Ile  
     420                       425                       430  
 Leu Leu Ala Gln Asp Thr Leu Asn Gln Asn Leu Asn Phe Glu Met Tyr  
     435                       440                       445  
 Gly Ala Val Tyr Ser Val Asn Pro Leu Asp Leu Pro Ala Ile Ile Glu  
     450                       455                       460  
 Arg Leu His Gly Leu Glu Ala Phe Ser Leu His Thr Tyr Ser Pro His  
     465                       470                       475                       480  
 Glu Leu Ser Arg Val Ala Ala Thr Leu Arg Lys Leu Gly Ala Pro Pro  
     485                       490                       495  
 Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu Ile  
     500                       505                       510  
 Ala Gln Gly Ala Arg Ala Ala Ile Cys Gly Arg Tyr Leu Phe Asn Trp  
     515                       520                       525

Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Ser Arg  
530 535 540  
Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly Asp Ile  
545 550 555 560  
Tyr His Ser Val Ser His Ala Arg Pro Arg Leu Leu Leu Cys Leu  
565 570 575  
Leu Leu Leu Ser Val Gly Val Gly Ile Phe Leu Leu Pro Asp Arg  
580 585 590

<210> 2  
<211> 1776  
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<220>  
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<221> variation  
<222> (3)...(3)  
<223> n = A or T

<221> variation  
<222> (9)...(9)  
<223> n = C or A

<221> variation  
<222> (13)...(13)  
<223> n = A or T

<221> variation  
<222> (15)...(15)  
<223> n = A or C

<221> variation  
<222> (21)...(21)  
<223> n = A or G

<221> variation  
<222> (24)...(24)  
<223> n = C or G

<221> variation  
<222> (28)...(28)  
<223> n = T or C

<221> modified\_base  
<222> (30)...(30)  
<223> n = G or C

<221> variation  
<222> (33)...(33)  
<223> n = C or A

<221> variation  
<222> (71)...(71)

<223> n = A or G

<221> variation

<222> (83)...(83)

<223> n = G or T

<221> variation

<222> (1174)...(1174)

<223> n = A or C

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acctcgagga gtcctctct	gagggcaaag aaggtgactt	ttgacaggggt gcaggtgctg	180
gacgcacact atgactcagt	cttgcaggac gttaaagcggg	ccgcctctaa gtttagtgcg	240
aggctcctca cggtagagga	agcctgcgcg ctgacccccgc	cccactccgc caaatcgcga	300
tacggatttgc	gggcaaaaga ggtgcgcagc	gggcccgttaa ccacatccgg	360
tccgtgtggg aggacctcct	ggaagaccaa cataccccaa	ttgacacaac tatcatggct	420
aaaaatgagg tggctgtcat	tgatccaact aaaggtggga	aaaagccagc tcgcctcatc	480
gtataccccg accttgggtt	cagggtgtgc gaaaagatgg	ccctctatga catgcacaa	540
aagcttccca aagcgataat	ggggccatcc tatgggttcc	aataactctcc cgccagaacgg	600
gtcgatttcc tcctcaaagc	ttggggaaat aagaaggacc	caatgggtt ctgttatgac	660
accgcgtct ttgactcaac	cgtcacggag agggacataa	gaacagaaga attccatata	720
caggcttgtt ctctgcctca	agaagccaga actgtcatac	actcgctcac tgagagactt	780
tacgttaggag ggcccatgac	aaacagcaaa gggcaatcct	gcggctacag gcgttgcgc	840
gcaagcgggtg ttttaccac	cagcatgggg aataccatga	catgttacat caaagccctt	900
gcagcgtgtt aggctgcagg	gatcgtggac cctgttatgt	tgggtgttgg agacgacctg	960
gtcgcatct cagagagcca	aggtaacgag gaggacgagc	gaaacctgag agctttcacg	1020
gaggctatga ccaggatttc	cgccccctcc ggtgaccttc	ccagaccgga atatgacttg	1080
gagcttataa catcctgctc	ctcaaacgta tcggtagcgc	tggactctcg gggtcgcgc	1140
cgtacttcc taaccagaga	ccctaccact ccantcaccc	gagctgttgg gaaaacagta	1200
agacactccc ctgtcaattc	ttggctgggc aacatcatcc	agtaccccc cacaatctgg	1260
gtccggatgg tcataatgac	tcacttcttc tccatactat	tggcccagga cactctgaac	1320
caaaatctca atttttagat	gtacggggca gtatactcgg	tcaatccatt agacctaccg	1380
gccataattt aaaggctaca	ttggcttgaa gcctttcac	tgcacacata ctctccccac	1440
gaactctcac gggtggcagc	aactctcaga aaacttggag	cgccctccct tagagcgtgg	1500
aagagtcggg cgcgtgcgt	gagagcttca ctcatgc(cc	aaggagcgag ggcggccatt	1560
tgtggccgct acctttcaa	ctggggcggtg aaaacaaaagc	tcaaactcac tccattgccc	1620
gaggcgagcc gcctggattt	atccgggtt ttcaccgtgg	gcccggcgg gggcgacatt	1680
tatcacagcg tgcgcatgc	ccgacccccc ctattactcc	tttgcctact cctacttagc	1740
gtaggagtag gcatctttt	actccccgat cgatga		1776

<210> 3

<211> 1394

<212> PRT

<213> Artificial Sequence

<220>

<223> modified NS3-5A

<221> VARIANT

<222> (1215)...(1215)

<223> Xaa = asparagine or serine

<221> VARIANT

&lt;222&gt; (904)...(904)

&lt;223&gt; Xaa = valine or alanine

&lt;400&gt; 3

Met Ala Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly  
 1                   5                   10                   15  
 Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly  
 20               25               30  
 Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys  
 35               40               45  
 Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr  
 50               55               60  
 Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp  
 65               70               75               80  
 Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr  
 85               90               95  
 Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala  
 100              105              110  
 Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu  
 115              120              125  
 Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu  
 130              135              140  
 Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys  
 145              150              155              160  
 Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met  
 165              170              175  
 Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro  
 180              185              190  
 Ala Val Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly  
 195              200              205  
 Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr  
 210              215              220  
 Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly  
 225              230              235              240  
 Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly  
 245              250              255  
 Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly  
 260              265              270  
 Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile  
 275              280              285  
 Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile  
 290              295              300  
 Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val  
 305              310              315              320  
 Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn  
 325              330              335  
 Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly  
 340              345              350  
 Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe  
 355              360              365  
 Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly  
 370              375              380  
 Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val  
 385              390              395              400

Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met  
 405 410 415  
 Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys  
 420 425 430  
 Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu  
 435 440 445  
 Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly  
 450 455 460  
 Arg Thr Gly Arg Gly Arg Met Gly Ile Tyr Arg Phe Val Thr Pro Gly  
 465 470 475 480  
 Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr  
 485 490 495  
 Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val  
 500 505 510  
 Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp  
 515 520 525  
 His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp  
 530 535 540  
 Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr  
 545 550 555 560  
 Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro  
 565 570 575  
 Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr  
 580 585 590  
 Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn  
 595 600 605  
 Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met  
 610 615 620  
 Ser Ala Asp Leu Glu Val Val Thr Ser Thr Trp Val Leu Val Gly Gly  
 625 630 635 640  
 Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Thr Thr Gly Ser Val Val  
 645 650 655  
 Ile Val Gly Arg Ile Ile Leu Ser Gly Arg Pro Ala Ile Val Pro Asp  
 660 665 670  
 Arg Glu Phe Leu Tyr Gln Glu Phe Asp Glu Met Glu Glu Cys Ala Ser  
 675 680 685  
 His Leu Pro Tyr Ile Glu Gln Gly Met Gln Leu Ala Glu Gln Phe Lys  
 690 695 700  
 Gln Lys Ala Leu Gly Leu Leu Gln Thr Ala Thr Lys Gln Ala Glu Ala  
 705 710 715 720  
 Ala Ala Pro Val Val Glu Ser Lys Trp Arg Ala Leu Glu Thr Phe Trp  
 725 730 735  
 Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile Gln Tyr Leu Ala Gly  
 740 745 750  
 Leu Ser Thr Leu Pro Gly Asn Pro Ala Ile Ala Ser Leu Met Ala Phe  
 755 760 765  
 Thr Ala Ser Ile Thr Ser Pro Leu Thr Thr Gln Ser Thr Leu Leu Phe  
 770 775 780  
 Asn Ile Leu Gly Gly Trp Val Ala Ala Gln Leu Ala Pro Pro Ser Ala  
 785 790 795 800  
 Ala Ser Ala Phe Val Gly Ala Gly Ile Ala Gly Ala Ala Val Gly Ser  
 805 810 815  
 Ile Gly Leu Gly Lys Val Leu Val Asp Ile Leu Ala Gly Tyr Gly Ala  
 820 825 830

Gly Val Ala Gly Ala Leu Val Ala Phe Lys Val Met Ser Gly Glu Met  
 835 840 845  
 Pro Ser Thr Glu Asp Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro  
 850 855 860  
 Gly Ala Leu Val Val Gly Val Val Cys Ala Ala Ile Leu Arg Arg His  
 865 870 875 880  
 Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala  
 885 890 895  
 Phe Ala Ser Arg Gly Asn His Xaa Ser Pro Thr His Tyr Val Pro Glu  
 900 905 910  
 Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu Thr Ile  
 915 920 925  
 Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu Asp Cys Ser  
 930 935 940  
 Thr Pro Cys Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys  
 945 950 955 960  
 Thr Val Leu Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro  
 965 970 975  
 Gln Leu Pro Gly Val Pro Phe Ser Cys Gln Arg Gly Tyr Lys Gly  
 980 985 990  
 Val Trp Arg Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala  
 995 1000 1005  
 Gln Ile Thr Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro  
 1010 1015 1020  
 Lys Thr Cys Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr  
 1025 1030 1035 1040  
 Thr Thr Gly Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr Ser Arg Ala  
 1045 1050 1055  
 Leu Trp Arg Val Ala Ala Glu Glu Tyr Val Glu Val Thr Arg Val Gly  
 1060 1065 1070  
 Asp Phe His Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro  
 1075 1080 1085  
 Cys Gln Val Pro Ala Pro Glu Phe Phe Thr Glu Val Asp Gly Val Arg  
 1090 1095 1100  
 Leu His Arg Tyr Ala Pro Ala Cys Arg Pro Leu Leu Arg Glu Glu Val  
 1105 1110 1115 1120  
 Thr Phe Gln Val Gly Leu Asn Gln Tyr Leu Val Gly Ser Gln Leu Pro  
 1125 1130 1135  
 Cys Glu Pro Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp  
 1140 1145 1150  
 Pro Ser His Ile Thr Ala Glu Thr Ala Lys Arg Arg Leu Ala Arg Gly  
 1155 1160 1165  
 Ser Pro Pro Ser Leu Ala Ser Ser Ser Ala Ile Gln Leu Ser Ala Pro  
 1170 1175 1180  
 Ser Leu Lys Ala Thr Cys Thr Thr His His Val Ser Pro Asp Ala Asp  
 1185 1190 1195 1200  
 Leu Ile Glu Ala Asn Leu Leu Trp Arg Gln Glu Met Gly Gly Xaa Ile  
 1205 1210 1215  
 Thr Arg Val Glu Ser Glu Asn Lys Val Val Val Leu Asp Ser Phe Asp  
 1220 1225 1230  
 Pro Leu Arg Ala Glu Glu Asp Glu Arg Glu Val Ser Val Pro Ala Glu  
 1235 1240 1245  
 Ile Leu Arg Lys Ser Lys Lys Phe Pro Ala Ala Met Pro Ile Trp Ala  
 1250 1255 1260

Arg Pro Asp Tyr Asn Pro Pro Leu Leu Glu Ser Trp Lys Asp Pro Asp  
 1265 1270 1275 1280  
 Tyr Val Pro Pro Val Val His Gly Cys Pro Leu Pro Pro Ile Lys Ala  
 1285 1290 1295  
 Pro Pro Ile Pro Pro Arg Arg Lys Arg Thr Val Val Leu Thr Glu  
 1300 1305 1310  
 Ser Ser Val Ser Ser Ala Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly  
 1315 1320 1325  
 Ser Ser Glu Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala Leu Pro  
 1330 1335 1340  
 Asp Gln Ala Ser Asp Asp Gly Asp Lys Gly Ser Asp Val Glu Ser Tyr  
 1345 1350 1355 1360  
 Ser Ser Met Pro Pro Leu Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser  
 1365 1370 1375  
 Asp Gly Ser Trp Ser Thr Val Ser Glu Glu Ala Ser Glu Asp Val Val  
 1380 1385 1390  
 Cys Cys

<210> 4  
 <211> 4182  
 <212> DNA  
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<220>  
 <223> modified NS3-5A

<221> variation  
 <222> (2711)...(2711)  
 <223> n = T or C

<221> variation  
 <222> (3645)...(3645)  
 <223> n = A or G

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 acacaatcct tcctggcgcac ctgcgtcaac ggctgtgtt ggaccgttta ccatgggtct 180  
 ggctcaaaga ccttagccgg cccaaagggg ccaatcaccc agatgtacac taatgtggac 240  
 caggacctcg tcggctggca ggcggcccccc ggggccccgtt ctttgacacc atgcacctgt 300  
 ggcagctcag acctttactt gtcacgaga catgttgacg tcattccgtt ggcggccgg 360  
 ggcgacagta gggggagcct gctctccccc aggctgtct cctacttgaa ggctcttcg 420  
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 acccgggggg ttgcgaaggc gttggacttt gtgcggcttag agtccatgga aactactatg 540  
 cggtctccgg tcttcacgga caactcatcc ccccccggccg taccgcagac attcaagt 600  
 gcccacctac acgctccac tggcagcggc aagagtacta aagtgcggc tgcatatgca 660  
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 gcccgtctta atactggaga gatccccttc tatggcaaag ccatccccat tgaagccatc 1080  
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<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 5

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34

<210> 6

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 6

atggagaaga aggtcattgt gtg

23

<210> 7

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<210> 8

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21

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 9

ctctcctcaa gcgtattcaa caagg

25

<210> 10

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 10

ccgtgcagcg taggttcag ccgta

25

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 11

cccattgtat gggatctgat ctgg

24

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<213> Artificial Sequence

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<223> primer

<400> 12

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28

<210> 13

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 13

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29

<210> 14

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 14

ggagaggata gcagggagt

19

<210> 15

<211> 29

<212> DNA

<213> Artificial Sequence

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<223> primer

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29

<210> 16

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 16

ggctggtgat agaggctgtg aatgccat

28

<210> 17

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> primer

<400> 17

ggatcaaatg tggaagtgtc tcatacgg

28

<210> 18

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<220>

<223> primer

<400> 18

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19

<210> 19

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 19

gcaatagcat cattgatggc attcacagc

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20

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21

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							20		25			30			
Gln	Asp	Ile	Gln	Pro	Ala	Ile	Gln	Ser	Ser	Trp	Pro	Lys	Leu	Glu	Gln
							35		40			45			
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							50		55			60			
Ala	Gly	Leu	Ser	Thr	Leu	Pro	Gly	Asn	Pro	Ala	Val	Ala	Ser	Met	Met
65							70		75			80			
Ala	Phe	Ser	Ala	Ala	Leu	Thr	Ser	Pro	Leu	Pro	Thr	Ser	Thr	Thr	Ile
							85		90			95			

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Ala Gly Ala Thr Gly Phe Val Val Ser Gly Leu Val Gly Ala Ala Val  
115 120 125  
Gly Ser Ile Gly Leu Gly Lys Ile Leu Val Asp Val Leu Ala Gly Tyr  
130 135 140  
Gly Ala Gly Ile Ser Gly Ala Leu Val Ala Phe Lys Ile Met Ser Gly  
145 150 155 160  
Glu Lys Pro Thr Val Glu Asp Val Val Asn Leu Leu Pro Ala Ile Leu  
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Arg His Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu  
195 200 205  
Ile Ala Phe Ala Ser Arg Gly Asn His Ala Ser Pro Thr His Tyr Val  
210 215 220  
Pro Glu Ser Asp Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu  
225 230 235 240  
Thr Ile Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu Asp  
245 250 255  
Cys Ser Thr Pro Cys  
260